



Mo5176new\_rev.txt

<110> Bayer Aktiengesellschaft

<120> Nucleic Acids which encode  
insect acetylcholine receptor subunits

<130> Le A 33 020-Foreign Countries

<140> US/09/303,232

<141> 1999-04-30

<150> DE 198 19 829.9

<151> 1998-05-04

<160> 14

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Drosophila melanogaster

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<221> CDS

<222> (372)..(2681)

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aaacaataaa gcatatactt gccatattga tataaaggga aatcgtgaaa aggcggtgaa 180  
aatttcgtaa gattagtttg tattaagggc agcccatgca cacagctaaa aagggaacta 240  
aaaaaacccc gcacagaaca atgaaagctg cagcagctgg ataaggccga caaaaccgaa 300  
aattatatta ttgtaatcta gtagagagca gacaacatat ccgctggcaa caaccaacac 360  
cgaaagagac t atg aaa aat gca caa ctg aaa ctg act gaa gtt gac gat 410  
Met Lys Asn Ala Gln Leu Lys Leu Thr Glu Val Asp Asp  
1 5 10  
gat gag ctg tgg ctg gca gta aga tta gcg cac tgc agc agc aac ttt 458  
Asp Glu Leu Trp Leu Ala Val Arg Leu Ala His Cys Ser Ser Asn Phe  
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agc agc agt agc agc aca aga acc acc agc agc aac cag agg cac aac 506  
Ser Ser Ser Ser Ser Thr Arg Thr Thr Ser Ser Asn Gln Arg His Asn  
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cag caa ctc aca aca ctg caa cca agg agc tta agt aca aaa cac cac 554  
Gln Gln Leu Thr Thr Leu Gln Pro Arg Ser Leu Ser Thr Lys His His  
50 55 60  
agc aac att gca agc gag cag cac aat agc cag caa cag gag cca gca 602  
Ser Asn Ile Ala Ser Glu Gln His Asn Ser Gln Gln Gln Glu Pro Ala  
65 70 75  
tcg aag gac gag gat gta gcc aac cac ggt aga agc aat gac cag cag 650  
Ser Lys Asp Glu Asp Val Ala Asn His Gly Arg Ser Asn Asp Gln Gln  
80 85 90

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gcc gca gca gca act gct gcc ggc gat gaa gca aca acc caa caa cca Ala Ala Ala Ala Thr Ala Ala Gly Asp Glu Ala Thr Thr Gln Gln Pro 110 115 120 125	746
aca aac ata aga ctg tgt gca cgc aag cga caa cga ttg cgt cgc cga Thr Asn Ile Arg Leu Cys Ala Arg Lys Arg Gln Arg Leu Arg Arg Arg 130 135 140	794
cga aaa aga aaa cca gca acc cca aac gaa aca gat atc aag aaa caa Arg Lys Arg Lys Pro Ala Thr Pro Asn Glu Thr Asp Ile Lys Lys Gln 145 150 155	842
cag caa ctt agc atg cct ccc ttc aaa acg cgc aaa tcc acg gac acc Gln Gln Leu Ser Met Pro Pro Phe Lys Thr Arg Lys Ser Thr Asp Thr 160 165 170	890
tac agc aca cca gca gca aca acc agc tgt ccg aca gcc acc tac atg Tyr Ser Thr Pro Ala Ala Thr Thr Ser Cys Pro Thr Ala Thr Tyr Met 175 180 185	938
caa tgt cga gcc agc gac aat gag ttc agt att ccg ata tcg aga cat Gln Cys Arg Ala Ser Asp Asn Glu Phe Ser Ile Pro Ile Ser Arg His 190 195 200 205	986
gat aga gta tcc acg gcc aca ttc gcc tgg gtg ttg cat gtg ctg cag Asp Arg Val Ser Thr Ala Thr Phe Ala Trp Val Leu His Val Leu Gln 210 215 220	1034
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tcg gtg cta ctg ttc aga agg atc gca gcg agc acc atc gcc ttc att Ser Val Leu Leu Phe Arg Arg Ile Ala Ala Ser Thr Ile Ala Phe Ile 240 245 250	1130
tcc tat tta ggc agc ttt gca gcg caa ctg aaa aat agc agc agc agc Ser Tyr Leu Gly Ser Phe Ala Ala Gln Leu Lys Asn Ser Ser Ser Ser 255 260 265	1178
agt agc agc agc aac agc agc aac aac agc agc acg caa ata tta aac Ser Ser Ser Ser Asn Ser Ser Asn Asn Ser Ser Thr Gln Ile Leu Asn 270 275 280 285	1226
gga ctt aat aaa cac tca tgg ata ttt tta ttg ata tat ttg aat tta Gly Leu Asn Lys His Ser Trp Ile Phe Leu Leu Ile Tyr Leu Asn Leu 290 295 300	1274
tct gct aaa gtt tgc cta gca gga tat cat gaa aag aga ctg tta cac Ser Ala Lys Val Cys Leu Ala Gly Tyr His Glu Lys Arg Leu Leu His 305 310 315	1322
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tcg gac ccg tta caa tta agc ttt ggt tta act tta atg caa att atc Ser Asp Pro Leu Gln Leu Ser Phe Gly Leu Thr Leu Met Gln Ile Ile 340 345 350	1418

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gga gtt aag gat ctg cga ata ccg ccg cat cgc atc tgg aag ccg gac Gly Val Lys Asp Leu Arg Ile Pro Pro His Arg Ile Trp Lys Pro Asp 385 390 395			1562
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ttc cag ctg gat tta caa tta caa gat gaa act ggc ggt gat atc agc Phe Gln Leu Asp Leu Gln Leu Gln Asp Glu Thr Gly Gly Asp Ile Ser 465 470 475			1802
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cgt aac gag atc tat tac aac tgc tgc ccg gaa ccc tat ata gac atc Arg Asn Glu Ile Tyr Tyr Asn Cys Cys Pro Glu Pro Tyr Ile Asp Ile 495 500 505			1898
acc ttc gcc atc atc atc cgc cga cga aca ctg tac tat ttc ttc aac Thr Phe Ala Ile Ile Ile Arg Arg Arg Thr Leu Tyr Tyr Phe Phe Asn 510 515 520 525			1946
ctg atc ata cct tgt gta ctg att gcc tcc atg gcc ttg ctc gga ttc Leu Ile Ile Pro Cys Val Leu Ile Ala Ser Met Ala Leu Leu Gly Phe 530 535 540			1994
acc ctg ccg cca gat tcg ggt gaa aaa tta tcg ctg ggt gtt acc atc Thr Leu Pro Pro Asp Ser Gly Glu Lys Leu Ser Leu Gly Val Thr Ile 545 550 555			2042
ttg ctc tcg ctg acc gtg ttt ctg aat atg gtt gcc gag aca atg ccg Leu Leu Ser Leu Thr Val Phe Leu Asn Met Val Ala Glu Thr Met Pro 560 565 570			2090
gct act tcc gat gcg gtg cca ttg tgg ata cgc atc gtg ttt ttg tgc Ala Thr Ser Asp Ala Val Pro Leu Trp Ile Arg Ile Val Phe Leu Cys 575 580 585			2138
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cac	cag	ata	ctc	tcc	gac	ggt	gag	ctg	aaa	gag	cgc	tcg	tcg	aaa	tcg	2282
His	Gln	Ile	Leu	Ser	Asp	Val	Glu	Leu	Lys	Glu	Arg	Ser	Ser	Lys	Ser	
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Leu	Leu	Ala	Asn	Val	Leu	Asp	Ile	Asp	Asp	Asp	Phe	Arg	His	Asn	Cys	
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Arg	Thr	Val	Tyr	Gly	Gln	Gly	Asp	Asp	Gly	Ser	Ile	Gly	Pro	Ile	Gly	
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Ser	Thr	Glu	Tyr	Glu	Leu	Gly	Leu	Ile	Leu	Lys	Glu	Ile	Arg	Phe	Ile	
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 65 70 75 80  
 Glu Asp Val Ala Asn His Gly Arg Ser Asn Asp Gln Gln Thr His Leu  
 85 90 95  
 Gln Gln Leu Asp Ser Ser Asn Met Leu Ser Pro Lys Thr Ala Ala Ala  
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 Ala Thr Ala Ala Gly Asp Glu Ala Thr Thr Gln Gln Pro Thr Asn Ile  
 115 120 125  
 Arg Leu Cys Ala Arg Lys Arg Gln Arg Leu Arg Arg Arg Arg Lys Arg  
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 Lys Pro Ala Thr Pro Asn Glu Thr Asp Ile Lys Lys Gln Gln Gln Leu  
 145 150 155 160  
 Ser Met Pro Pro Phe Lys Thr Arg Lys Ser Thr Asp Thr Tyr Ser Thr  
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 Pro Ala Ala Thr Thr Ser Cys Pro Thr Ala Thr Tyr Met Gln Cys Arg  
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 Ala Ser Asp Asn Glu Phe Ser Ile Pro Ile Ser Arg His Asp Arg Val  
 195 200 205  
 Ser Thr Ala Thr Phe Ala Trp Val Leu His Val Leu Gln Val Leu Leu  
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 Val Ser Leu Gln Gln Trp Gln Leu His Val Gln Gln Arg Ser Val Leu  
 225 230 235 240  
 Leu Phe Arg Arg Ile Ala Ala Ser Thr Ile Ala Phe Ile Ser Tyr Leu  
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 Gly Ser Phe Ala Ala Gln Leu Lys Asn Ser Ser Ser Ser Ser Ser Ser  
 260 265 270  
 Ser Asn Ser Ser Asn Asn Ser Ser Thr Gln Ile Leu Asn Gly Leu Asn  
 275 280 285  
 Lys His Ser Trp Ile Phe Leu Leu Ile Tyr Leu Asn Leu Ser Ala Lys  
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 325 330 335  
 Leu Gln Leu Ser Phe Gly Leu Thr Leu Met Gln Ile Ile Asp Val Asp  
 340 345 350

Glu Lys Asn Gln Leu Leu Val Thr Asn Val Trp Leu Lys Leu Glu Trp  
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 Ile Tyr Tyr Asn Cys Cys Pro Glu Pro Tyr Ile Asp Ile Thr Phe Ala  
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 625 630 635 640  
 Asn Val Leu Asp Ile Asp Asp Asp Phe Arg His Asn Cys Arg Pro Met  
 645 650 655  
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 Tyr Gly Gln Gly Asp Asp Gly Ser Ile Gly Pro Ile Gly Ser Thr Arg  
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Leu Arg Lys Asp Asp Glu Cys Asn Asp Ile Ala Asn Asp Trp Lys Phe  
725 730 735  
Ala Ala Met Val Val Asp Arg Leu Cys Leu Ile Ile Phe Thr Met Phe  
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gcggcgcgcg gcgcggcggc gtcgcggcgc tgac atg ggc ggg cgg gcg cgc cgc 355  
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tcg cac ttg gcg gcg ccc gcg ggc ctg ctg ctg ctg tgc ctg ctc 403  
Ser His Leu Ala Ala Pro Ala Gly Leu Leu Leu Leu Cys Leu Leu  
10 15 20  
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Trp Pro Arg Gly Ala Arg Cys Gly Tyr His Glu Lys Arg Leu Leu His  
25 30 35  
cac cta ttg gac cac tac aac gta ctg gag agg ccc gtc gtc aac gag 499  
His Leu Leu Asp His Tyr Asn Val Leu Glu Arg Pro Val Val Asn Glu  
40 45 50 55  
agc gac ccg ctg cag ctc tcc ttc ggc ctc acg ctc atg cag atc atc 547  
Ser Asp Pro Leu Gln Leu Ser Phe Gly Leu Thr Leu Met Gln Ile Ile  
60 65 70  
gac gtg gac gag aag aac cag ctt tta ata aca aac atc tgg cta aaa 595  
Asp Val Asp Glu Lys Asn Gln Leu Leu Ile Thr Asn Ile Trp Leu Lys  
75 80 85

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ggg	gtc	aaa	gat	tta	aga	gtg	cca	ccc	cac	aga	cta	tgg	aaa	cca	gac	691
Gly	Val	Lys	Asp	Leu	Arg	Val	Pro	Pro	His	Arg	Leu	Trp	Lys	Pro	Asp	
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gtc	ctt	atg	tac	aac	agc	gcg	gac	gaa	ggg	ttc	gac	agc	acg	tat	cca	739
Val	Leu	Met	Tyr	Asn	Ser	Ala	Asp	Glu	Gly	Phe	Asp	Ser	Thr	Tyr	Pro	
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acg	aac	gtg	gtg	gtg	cgg	aac	aac	ggc	tcg	tgt	ctg	tac	gtg	ccg	ccc	787
Thr	Asn	Val	Val	Val	Arg	Asn	Asn	Gly	Ser	Cys	Leu	Tyr	Val	Pro	Pro	
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ggc	atc	ttc	aag	agc	acc	tgc	aag	atc	gac	atc	acc	tgg	ttc	ccc	ttc	835
Gly	Ile	Phe	Lys	Ser	Thr	Cys	Lys	Ile	Asp	Ile	Thr	Trp	Phe	Pro	Phe	
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gac	gac	caa	cga	tgc	gag	atg	aag	ttt	ggc	agc	tgg	act	tat	gat	ggc	883
Asp	Asp	Gln	Arg	Cys	Glu	Met	Lys	Phe	Gly	Ser	Trp	Thr	Tyr	Asp	Gly	
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tat	cag	ttg	gat	cta	caa	cta	cag	gat	gaa	ggg	ggc	gga	gat	ata	agc	931
Tyr	Gln	Leu	Asp	Leu	Gln	Leu	Gln	Asp	Glu	Gly	Gly	Gly	Asp	Ile	Ser	
	185					190					195					
agt	ttt	gtc	acg	aat	ggc	gaa	tgg	gag	tta	ata	gga	gtc	ccc	ggc	aag	979
Ser	Phe	Val	Thr	Asn	Gly	Glu	Trp	Glu	Leu	Ile	Gly	Val	Pro	Gly	Lys	
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cgc	aac	gag	atc	tac	tac	aac	tgt	tgt	ccg	gag	cca	tac	atc	gac	atc	1027
Arg	Asn	Glu	Ile	Tyr	Tyr	Asn	Cys	Cys	Pro	Glu	Pro	Tyr	Ile	Asp	Ile	
				220					225					230		
acg	ttt	gcg	gtg	gtg	atc	cgg	agg	aaa	acg	ctc	tac	tac	ttc	ttc	aat	1075
Thr	Phe	Ala	Val	Val	Ile	Arg	Arg	Lys	Thr	Leu	Tyr	Tyr	Phe	Phe	Asn	
			235					240					245			
ctg	atc	gtg	ccc	tgc	gtg	ctc	atc	gcc	tcc	atg	gct	cta	ttg	ggg	ttc	1123
Leu	Ile	Val	Pro	Cys	Val	Leu	Ile	Ala	Ser	Met	Ala	Leu	Leu	Gly	Phe	
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acc	ttg	cct	cca	gac	tcc	gga	gaa	aag	ttg	tct	tta	ggt	gtg	acg	ata	1171
Thr	Leu	Pro	Pro	Asp	Ser	Gly	Glu	Lys	Leu	Ser	Leu	Gly	Val	Thr	Ile	
	265					270					275					
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Leu	Leu	Ser	Leu	Thr	Val	Phe	Leu	Asn	Met	Val	Ala	Glu	Thr	Met	Pro	
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gcg	acg	tcg	gac	gcc	gtg	ccc	ttg	ctc	ggc	acc	tac	ttc	aac	tgc	atc	1267
Ala	Thr	Ser	Asp	Ala	Val	Pro	Leu	Leu	Gly	Thr	Tyr	Phe	Asn	Cys	Ile	
				300					305					310		
atg	ttc	atg	gtg	gct	tcc	tcc	gtc	gtc	tcc	acc	ata	ctg	atc	ctc	aac	1315
Met	Phe	Met	Val	Ala	Ser	Ser	Val	Val	Ser	Thr	Ile	Leu	Ile	Leu	Asn	
			315					320					325			
tac	cac	cac	cgg	cac	gca	gac	act	cac	gaa	atg	agt	gat	tgg	att	cgt	1363
Tyr	His	His	Arg	His	Ala	Asp	Thr	His	Glu	Met	Ser	Asp	Trp	Ile	Arg	



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ctg gag ctg cgc gag cgc tcc tcc aag tcg ctc cta gcg aac gtg ctc 1507	Leu Glu Leu Arg Glu Arg Ser Ser Lys Ser Leu Leu Ala Asn Val Leu	380 385 390	
gac atc gat gac gac ttc cgc cac ccg caa gcg cag cag ccg caa tgc 1555	Asp Ile Asp Asp Asp Phe Arg His Pro Gln Ala Gln Gln Pro Gln Cys	395 400 405	
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<213> *Heliothis virescens*

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 Pro Val Ala Asn Glu Ser Glu Pro Leu Glu Val Arg Phe Gly Leu Thr  
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 Asp Ser Glu Tyr Gly Gly Val Lys Asp Leu Arg Ile Thr Pro Asn Lys  
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<220>  
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